

RAW SEQUENCE LISTING PATENT APPLICATION US/09/477,392

OIPE

DATE: 01/31/2000
TIME: 11:06:53

Input Set: I477392.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Heintz, Nicholas
2 Houchens, Christopher
3 <120> TITLE OF INVENTION: RIP60 Nucleic Acid and Polypeptide
4 Sequences and Uses Therefor
5 <130> FILE REFERENCE: V0139/7038 (HCL/MAT)
6 <140> CURRENT APPLICATION NUMBER: US/09/477,392
7 <141> CURRENT FILING DATE: 2000-01-04
8 <150> EARLIER APPLICATION NUMBER: US 60/114,745
9 <151> EARLIER FILING DATE: 1999-01-04
10 <150> EARLIER APPLICATION NUMBER: US 60/114,743
11 <151> EARLIER FILING DATE: 1999-01-04
12 <160> NUMBER OF SEQ ID NOS: 68
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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15 <211> LENGTH: 2954
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo Sapiens
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20 <222> LOCATION: (130)...(1831)
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24 gaagaaccg atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg ggc ctg 171
25 Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu
26 1 5 10
27 gcc cag ccc cga ctc ctt tct ggg ccc tcc cag gag tca ccc cag acc 219
28 Ala Gln Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr
29 15 20 25 30
30 ctg ggg aag gag tcc cgc ggg ctg agg caa caa ggc acg tca gtg gcc 267
31 Leu Gly Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala
32 35 40 45
33 cag tct ggt gcc caa gcc cca ggc agg gcc cat cgc tgt gcc cac tgt 315
34 Gln Ser Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys
35 50 55 60
36 cga agg cac ttc cct ggc tgg gtg gct ctg tgg ctt cac acc cgc cgg 363
37 Arg Arg His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg
38 65 70 75
39 tgc cag gcc cgg ctg ccc ttg ccc tgc cct gag tgt ggc cgt cgc ttt 411
40 Cys Gln Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe
41 80 85 90
42 cgc cat gcc ccc ttc tta gca ctg cac cgc cag gtc cat gct gct gcc 459
43 Arg His Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala
44 95 100 105 110

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47	115 120 125	
48	ggc tgg gtg gcc ctg gtt ctg cat ctg ctg gcc cat tca gct gca aag	555
49	Gly Trp Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys	
50	130 135 140	
51	caa ccc atc gct tgt ccc aaa tgc gag aga cgc ttc tgg cga cga aag	603
52	Gln Pro Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys	
53	145 150 155	
54	cag ctt cga gct cat ctg cgg cgg tgc cac cct ccc gcc ccg gag gcc	651
55	Gln Leu Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala	
56	160 165 170	
57	cgg ccc ttc ata tgc ggc aac tgt ggc cgg agc ttt gcc cag tgg gac	699
58	Arg Pro Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp	
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62	195 200 205	
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65	210 215 220	
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67	Thr Ala Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys	
68	225 230 235	
69	gcc tgt tgt ggc aag cgc ttc cgg cac aag ccc aac ttg atc gct cac	891
70	Ala Cys Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His	
71	240 245 250	
72	cgc cgc gtg cac acg ggc gag cgg ccc cac cag tgc ccc gag tgc ggg	939
73	Arg Arg Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly	
74	255 260 265 270	
75	aag cgc ttt acc aat aag ccc tat ctg act tcg cac cgg cgc atc cac	987
76	Lys Arg Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His	
77	275 280 285	
78	acc ggc gag aag ccc tac ccg tgc aaa gag tgc ggc cgc cgc ttc cgg	1035
79	Thr Gly Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg	
80	290 295 300	
81	cac aaa ccc aac ctg ctg tct cac agc aag att cac aag cga tcc gag	1083
82	His Lys Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu	
83	305 310 315	
84	ggg tcg gcc cag gcc gcc ccc ggc ccg ggg agc ccc cag ctg cca gcc	1131
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87	ggc ccc cag gag tcc gcg gcc gag ccc acc ccg gcg gta cct ctg aaa	1179
88	Gly Pro Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys	
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90	ccg gcc cag gag ccg ccg cca ggg gcc ccg cca gag cac ccg cag gac	1227
91	Pro Ala Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp	
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93	ccg atc gaa gcc ccc ccc tcc ctc tac agc tgc gac gac tgc ggc agg	1275
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95					370					375					380					
96	agc	ttc	cgg	ctg	gag	cgc	ttc	ctg	cgg	gcc	cac	cag	cgg	cac	gac	acc				1323
97	Ser	Phe	Arg	Leu	Glu	Arg	Phe	Leu	Arg	Ala	His	Gln	Arg	His	Asp	Thr				
98			385						390				395							
99	ggg	gag	cgg	ccc	ttc	acc	tgc	gcc	gag	tgc	ggg	aag	aac	ttc	ggc	aag				1371
100	Gly	Glu	Arg	Pro	Phe	Thr	Cys	Ala	Glu	Cys	Gly	Lys	Asn	Phe	Gly	Lys				
101		400					405					410								
102	aag	acg	cac	ctg	gtg	gcg	cac	tcg	ccg	gtg	cac	tcc	ggc	gag	cgg	ccc				1419
103	Lys	Thr	His	Leu	Val	Ala	His	Ser	Pro	Val	His	Ser	Gly	Glu	Arg	Pro				
104		415				420					425				430					
105	ttc	gcc	tgc	gag	gag	tgc	ggc	cgc	cgc	ttc	tcc	cag	ggc	agc	cat	ctg				1467
106	Phe	Ala	Cys	Glu	Glu	Cys	Gly	Arg	Arg	Phe	Ser	Gln	Gly	Ser	His	Leu				
107			435						440			445								
108	gcg	gcg	cat	cgg	ccg	gac	cac	gcc	ccc	gat	cgg	ccc	ttc	gtg	tgt	ccc				1515
109	Ala	Ala	His	Arg	Pro	Asp	His	Ala	Pro	Asp	Arg	Pro	Phe	Val	Cys	Pro				
110			450						455			460								
111	gac	tgc	ggc	aag	gcc	ttc	cgc	cac	aaa	ccc	tac	ctg	gcg	cgg	cac	cgg				1563
112	Asp	Cys	Gly	Lys	Ala	Phe	Arg	His	Lys	Pro	Tyr	Leu	Ala	Arg	His	Arg				
113			465				470				475									
114	cgc	atc	cac	acc	ggc	gag	aag	ccc	tac	gtc	tgc	ccc	gac	tgc	ggc	aaa				1611
115	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Val	Cys	Pro	Asp	Cys	Gly	Lys				
116		480				485					490									
117	gcc	ttc	agc	cag	aag	tcc	aac	ctg	gtg	tcg	cac	cgg	cgc	atc	cac	acg				1659
118	Ala	Phe	Ser	Gln	Lys	Ser	Asn	Leu	Val	Ser	His	Arg	Arg	Ile	His	Thr				
119		495				500					505				510					
120	ggc	gag	cgg	ccc	tac	gcc	tgt	ccc	gac	tgc	gac	cgc	agc	ttc	agc	cag				1707
121	Gly	Glu	Arg	Pro	Tyr	Ala	Cys	Pro	Asp	Cys	Asp	Arg	Ser	Phe	Ser	Gln				
122			515						520			525								
123	aag	tcc	aac	ctc	atc	acc	cac	cgc	aag	agc	cac	atc	cgg	gac	ggc	gcc				1755
124	Lys	Ser	Asn	Leu	Ile	Thr	His	Arg	Lys	Ser	His	Ile	Arg	Asp	Gly	Ala				
125			530						535			540								
126	ttc	tgc	tgt	gcc	atc	tgt	ggc	cag	acc	ttc	gac	gac	gag	gag	aga	ctc				1803
127	Phe	Cys	Cys	Ala	Ile	Cys	Gly	Gln	Thr	Phe	Asp	Asp	Glu	Glu	Arg	Leu				
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129	ctg	gcc	cac	cag	aag	aag	cac	gat	gtc	t	gagacggttg	gcggggccgt								1851
130	Leu	Ala	His	Gln	Lys	Lys	His	Asp	Val											
131		560					565													
132	gttggctgag	agagggctgg	ggtccttcgt	ggtgggagtc	gcagtgggct	gggggtgcct														1911
133	gcctagtgt	ggagtagggg	acaatgggaa	tcctagaggg	gatggaagat	gcggggagtg														1971
134	agctgggttg	gccctgctag	cgagagaggt	caaccccgg	ggccagggaa	cccacttcca														2031
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137	ggaaaggaag	ccctccatcc	tctggtatta	acgccttaat	gccccctgtct	tttactgtaa														2211
138	gttacttaga	tcatTTTTTg	aagcaggcgt	ggtagagtcc	tgtaaataaa	tgctctgggc														2271
139	tagatacagc	ttggagaacc	tgctggcctt	gtagacaga	acttgggcct	ttgccagcag														2331
140	caagaggtga	agcgaagcca	ctcttacctc	tcccttcccc	tcccacctgc	cccctgcgta														2391
141	ggcaccacaga	cttgagagaga	cccgtctgct	gttaataactt	ccatcctctt	ccttcccaaa														2451
142	gagcagatcc	caaggcattt	actccttggt	ctgtctcgct	ttatctgtcg	cccctcccag														2511
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147      gatgattcta attgttagaa attctaattg ttagaaatcc ttctttataa tgaatgaatt      2811
148      ctgcttttctt ataatttcta cctattgggc cttgtttctgt tctctggaac taaacagaac      2871
149      aaccattttac ccctcctttt caaactagag aataaacatt tggtttttaga aaaaaaaaaa      2931
150      aaaaaaaaaa aaaaaaaaaa aaa                                     2954
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152      <211> LENGTH: 567
153      <212> TYPE: PRT
154      <213> ORGANISM: Homo Sapiens
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159      20          25          30
160      Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala Gln Ser
161      35          40          45
162      Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys Arg Arg
163      50          55          60
164      His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln
165      65          70          75          80
166      Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His
167      85          90          95
168      Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala Thr Pro
169      100         105         110
170      Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp
171      115         120         125
172      Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys Gln Pro
173      130         135         140
174      Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu
175      145         150         155         160
176      Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro
177      165         170         175
178      Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu
179      180         185         190
180      Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu Ala Ala
181      195         200         205
182      Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala
183      210         215         220
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185      225         230         235         240
186      Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg
187      245         250         255
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189      260         265         270
190      Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly
191      275         280         285
192      Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys
193      290         295         300
194      Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser

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197      325      330      335
198      Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala
199      340      345      350
200      Gln Glu Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile
201      355      360      365
202      Glu Ala Pro Pro Ser Leu Tyr Ser Cys Asp Asp Cys Gly Arg Ser Phe
203      370      375      380
204      Arg Leu Glu Arg Phe Leu Arg Ala His Gln Arg His Asp Thr Gly Glu
205      385      390      395      400
206      Arg Pro Phe Thr Cys Ala Glu Cys Gly Lys Asn Phe Gly Lys Lys Thr
207      405      410      415
208      His Leu Val Ala His Ser Pro Val His Ser Gly Glu Arg Pro Phe Ala
209      420      425      430
210      Cys Glu Glu Cys Gly Arg Arg Phe Ser Gln Gly Ser His Leu Ala Ala
211      435      440      445
212      His Arg Pro Asp His Ala Pro Asp Arg Pro Phe Val Cys Pro Asp Cys
213      450      455      460
214      Gly Lys Ala Phe Arg His Lys Pro Tyr Leu Ala Arg His Arg Arg Ile
215      465      470      475      480
216      His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys Ala Phe
217      485      490      495
218      Ser Gln Lys Ser Asn Leu Val Ser His Arg Arg Ile His Thr Gly Glu
219      500      505      510
220      Arg Pro Tyr Ala Cys Pro Asp Cys Asp Arg Ser Phe Ser Gln Lys Ser
221      515      520      525
222      Asn Leu Ile Thr His Arg Lys Ser His Ile Arg Asp Gly Ala Phe Cys
223      530      535      540
224      Cys Ala Ile Cys Gly Gln Thr Phe Asp Asp Glu Glu Arg Leu Leu Ala
225      545      550      555      560
226      His Gln Lys Lys His Asp Val
227      565

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228 <210> SEQ ID NO 3

229 <211> LENGTH: 378

230 <212> TYPE: DNA

231 <213> ORGANISM: Homo Sapiens

232 <220> FEATURE:

233 <221> NAME/KEY: CDS

234 <222> LOCATION: (1)...(378)

235 <400> SEQUENCE: 3

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238      1      5      10      15
239      cgc ttc cgg cac aag ccc aac ttg atc gct cac cgc cgc gtg cac acg      96
240      Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg Val His Thr
241      20      25      30
242      ggc gag cgg ccc cac cag tgc ccc gag tgc ggg aag cgc ttt acc aat      144
243      Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg Phe Thr Asn
244      35      40      45

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I477392.RAW

Line	Error/Warning	Original Text
680	W "N" or "Xaa" used: Feature required	Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe X
682	W "N" or "Xaa" used: Feature required	Xaa Xaa His Xaa Xaa Xaa His Xaa